

Figure 1A

1	CAAGGTTCTGAAGGAARCAAGGTCAAGAGGCATCCTGCATGTATGGGGCAAACCTGCTAT	60
61	AGGAAGAATCCTGTTCAATTTTCAACATTTTAGCCATCCTGGTGATAGTGATTATGGAGGT	120
121	GTACAAATCGTGGGCCAAGATGAGACTGATGACCGGCTGAATGTCCCTATGGACCATCC	180
181	TGTTATAGGAAGAATCCCCAGCACAGAATAGAAATATAGACATAATACGCTTCCAGTGAGA	240
241	AATGTTTTAGATGAAGATAATGATAATGTTGGGCAACCAATGAGTATGACCTGAACGAC	300
301	AGCTTCTAGATGATGAGGAAGAAGACTATGAGCCAACAGATGAAGATTCTGACTGGGAA	360
361	CCAGGAAAGGAAGATGAAGAGAAGGAAGATGTGGAAGAGCTTTGAAAGAAGCAAAAAGC	420
421	AAATAATTTCCCGCATCTTCACTCTTCATCTTCCACCCCTCTTCTGGACAACCTTGACA	480
481	TTCTGTGATATTGACATTCACCATAAACATTGCATGATTCAGTTCTCCTTGATATCTTG	540
541	GTGCTTGGACTCTTCACTGTGGCATCATTAGGTCAGCAGGTGAACACTCAGGATTGTTT	600
601	CTCTTCTGTTAGTAGAGACCAAAAGACAGGGTCTGGCTCTGTCACCTAAGCCAGAGGGC	660
661	AATGGTACAATCACCATTGACTGCAGTCTCAAATTCCTGGGCTCAAGCAATCTCCCGCC	720
721	TCAGCTTCCCAAGCAGCTGGGACTACAGGCATGCCCCACCATGTCAGGGAATGGTGCT	780
781	GGACCCAGAGAATAACTGGATCTTCAAGGAAGGAAGAGAAATCTTCAGAAGAACATGGAT	840
841	TTTCCCCACTGGTAGTTAGTTGTCTCTTCATATCCAGAAATAACTTGAACACGTTAGAC	900
901	GGGGCCACTGTGCATAGTGTCTCCAGGAAAACGCCAAGATTCTCCAAGACACTTTCAT	960
961	ATCCTAAGCCCTGTTCTGTTTGTCTTGTGTAGTAAATTGGCAAATTTGCGAGTACAGAA	1020
1021	GACATCTCTAACTGATGTCACAAAGAATCATGTCTGSGCCATACAAAGTATTCTAACTA	1080
1081	ACCATGTAAGCCACTAGAATGTTAAACTAATGCTCTGGCACTGAGGTTTGAATGGAGCT	1140

Figure 1B

1141 CAGATACCATACCCCAAAGATGCTGGCAGAGACATTCTGACTCATTAAAGGGAGAGCTGGC 1200

1201 TGATAGCAGAGAGGGGTGACATCAGCCTTGACAGACATTGCCCTGGGGAATTCTGAGCAGT 1260

1261 GTTGCTCACAGCACCACTGGCCAGATGGAGACCACCATGGGGTTCATGGATGACAATGC 1320
 1 M E T T M G F M D D N A 12

1321 CACCAACACTTCCACCAGCTTCTTTCTGTGCTCAACCCATCATGGAGCCCATGCCACTTC 1380
 13 T N T S T S F L S V L N P H G A H A T S 32

1381 CTTCCCATTCAACTTCAGCTACAGCGACTATGATATGCCTTTGGATGAAGATGAGGATGT 1440
 33 F P F N F S Y S D Y D M P L D E D E D V 52

1441 GACCAATTCAGGACGTTCTTTGCTGCCAAGATTGTCATTGGGATGGCCCTGGTGGGCAT 1500
 53 T N S R T F F A A K I V I G M A L V G I 72

1501 CATGCTGGTCTGCGGCATTTGAACTTCATCTTTATCGCTGCCCTGGTCCCTACAAGAA 1560
 73 M L V C G I G N F I F I A A L V R Y K K 92

1561 ACTGCGCAACCTCACCAACCTGCTCATCGCAACCTGGCCATCTCTGACTTCCTGGTGGC 1620
 93 L R N L T N L L I A N L A I S D F L V A 112

1621 CATGTGCTGCTGCCCTTTGAGATGGACTACTATGTGGTGGCCAGCTCTCTGGGAGCA 1680
 113 I V C P F E M D Y Y V V R Q L S W E H 132

1681 CGGCCACGTCTGTGCACCTCTGTCAACTACCTGCGCACTGTCTCTCTATGTCTCCAC 1740
 133 G H V L T S V N Y L R T V S L Y V S T 152

1741 CAATGCCCTGTGGCCATCGCCATTGACAGGTATCTGGCTATTGTCCATCCGCTGAGACC 1800
 153 N A L L A I A I D R Y L A I V H P L R P 172

1801 ACGGATGAAGTGCCAAACAGCCATGGCCTGATTGCCTTGGTGTGGACGGTGTCCATCCT 1860
 173 R M K C Q T A T G L I A L V W T V S I L 192

1861 GATCGCCATCCCTTCCGCTACTTCAACCCGAGACGGTCTCTGTCATTGTCAAGACCA 1920
 193 I A I P S A Y F T T E T V L V I V K S Q 212

1921 GGAAAAGATCTTCTGCGGCCAGATCTGGCTGTGGACCAAGCTCTACTACAAGTCCTA 1980
 213 E K I F G Q I W P V D Q Q L Y Y K S Y 232

1981 CTTCTCTTTATCTTTGGCATAGAATTCGTGGGCCCGTGGTCACCATGACCCCTGTGCTA 2040
 233 F L F I F G I E F V G P V V T M T L C Y 252

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Figure 1C

2041 TGCCAGGATCTCCCGGGAGCTCTGGTTCAAGGCGGTCCCTGGATTCCAGACAGAGCAGAT 2100
 253 A R I S R E L W F K A V P G F Q T E Q I 272

2101 CCGCAAGAGGCTGCGCTGCGCGAGGAAGACGGTCTGCTGCTCATGTGCATCTCACC GC 2160
 273 R K R L R L **C** R R K T V L V L M **I** L T A 292

2161 CTACGTGCTATGCTGGGCGCCCTTCTACGGCTTCACCATCGTGCGGACTTCTTCCCCAC 2220
 293 Y V L C W A P F Y G F T I V R D F F P T 312

2221 CGTGTTTTGTAAGGAGAAGCACTACCTCACTGCCTTCTACATCGTCGAGTGCATCGCCAT 2280
 313 V F V K E K H Y L T A F Y I V E C I A M 332

2281 GAGCAACAGCATGATCAACACTCTGTGCTTCGTGACCGTCAAGAAGCACACCGTCAAGTA 2340
 333 S N S M I N T L C F V T V K N D T V K Y 352

2341 CTTCAAAAAGATCATGTTGCTCCTGGAAGGCTTCTTACAATGGCGGTAAGTCCAGTGC 2400
 353 F K K I M L L H W K A S Y N G G K S S A 372

2401 AGACCTGGACCTCAAGACAATTGGGATGCCTGCCACCGAAGAGGTGGACTGCATCAGACT 2460
 373 D L D L K T I G M P A T E E V D C I R L 392

2461 AAAATAACCCCTGGACTTTGCAAAGTTTAAACACAAAGCAGGGTCTGTGGACACTGAC 2520
 393 K * 394

2521 TAGTGTGCTTGGATGCACATCAACCTGGAACTTTTTGTGTTGCTGCAGAGGGTAAAGTAAA 2580

2581 TGGACCACTCTGTGAAA 2640

2641 AAAAAAAAAAAAAA 2654

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Figure 2

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HGRBPMY14      METTTCGNDNDNTNTTSFSLILNPHGAGHATSFPPNLSVDVLPDLEDEDRKRTFFFA
human_gpcr_dJ60N4_3
gpcr73_mouse   VCVDFVLPDLEDEDRKRTFFFA
NPY2R_chicken  METTTCGNDNTNTTSFSLILNPHGAGHATSGLSLFTVLPDVLPDLEDEDRKRTFFFA
NPY2R_rat       TCGTCAETGEGGDEKRLK...RLPTKLTLPLPRTMADPKPKDKKSLHIVE
HGRBPMY14      TCGTCAETGEGGDEKRLK...SLYGS...GP...TFTGRTCTP...PRTKIDRLKTL
human_gpcr_dJ60N4_3
gpcr73_mouse   AKTGVIALNTLMVCGGICNFFLAKRKRLRNLTLNLNLANSIFVATLCCPCEFA
NPY2R_chicken  AKTGVIALNTLMVCGGICNFFLAKRKRLRNLTLNLNLANSIDPVLVATLCCPCEFA
NPY2R_rat       AKTGVIALNTLMVCGICNFFLAKRKRLRNLTLNLNLANSIDPVLVATLCCPCEFA
HGRBPMY14      VAVTLITVPGCSLTLGGVGSNSVHVHVKRSSTVTFITANLIDLVAVTICPITPL
human_gpcr_dJ60N4_3
gpcr73_mouse   VAVTLITVPGCSLTLGGVGSNSVHVHVKRSSTVTFITANLIDLVAVTICPITPL
NPY2R_chicken  DYYVTVVOLSNEHGHVLCISVNLKRLTVSLVYSTNALLAIAIDRYLAIVHPLPRKCKOTAT
NPY2R_rat       DYYVTVVOLSNEHGHVLCISVNLKRLTVSLVYSTNALLAIAIDRYLAIVHPLPRKCKOTAT
HGRBPMY14      GGLFVHNVSLILAIISAYETVETVIVKRSKIFGCGQVWVDDQVLYSSVETVIFGCI
human_gpcr_dJ60N4_3
gpcr73_mouse   GGLFVHNVSLILAIISAYETVETVIVKRSKIFGCGQVWVDDQVLYSSVETVIFGCI
NPY2R_chicken  GGLFVHNVSLILAIISAYETVETVIVVREKRTFCGQVWVDDQVLYSSVETVIFGCI
NPY2R_rat       LITLHNVSLILAIISAYETVETVIVVREKRTFCGQVWVDDQVLYSSVETVIFGCI
HGRBPMY14      LITLHNVSLILAIISAYETVETVIVVREKRTFCGQVWVDDQVLYSSVETVIFGCI
human_gpcr_dJ60N4_3
gpcr73_mouse   LITLHNVSLILAIISAYETVETVIVVREKRTFCGQVWVDDQVLYSSVETVIFGCI
NPY2R_chicken  LITLHNVSLILAIISAYETVETVIVVREKRTFCGQVWVDDQVLYSSVETVIFGCI
NPY2R_rat       LITLHNVSLILAIISAYETVETVIVVREKRTFCGQVWVDDQVLYSSVETVIFGCI
HGRBPMY14      CFVGVVVVITLVCARISRELVKFAVVGTEQFQTLKRCRRTVILVLCVAVLCWAR
human_gpcr_dJ60N4_3
gpcr73_mouse   CFVGVVVVITLVCARISRELVKFAVVGTEQFQTLKRCRRTVILVLCVAVLCWAR
NPY2R_chicken  CFVGVVVVITLVCARISRELVKFAVVGTEQFQTLKRCRRTVILVLCVAVLCWAR
NPY2R_rat       CFVGVVVVITLVCARISRELVKFAVVGTEQFQTLKRCRRTVILVLCVAVLCWAR
HGRBPMY14      LITLHNVSLILAIISAYETVETVIVVREKRTFCGQVWVDDQVLYSSVETVIFGCI
human_gpcr_dJ60N4_3
gpcr73_mouse   LITLHNVSLILAIISAYETVETVIVVREKRTFCGQVWVDDQVLYSSVETVIFGCI
NPY2R_chicken  LITLHNVSLILAIISAYETVETVIVVREKRTFCGQVWVDDQVLYSSVETVIFGCI
NPY2R_rat       LITLHNVSLILAIISAYETVETVIVVREKRTFCGQVWVDDQVLYSSVETVIFGCI
HGRBPMY14      FVGFVTVVDFEFTVVEVKRHHYLAALFETLHNSMSINLCFTVTVNNHNYA.....
human_gpcr_dJ60N4_3
gpcr73_mouse   FVGFVTVVDFEFTVVEVKRHHYLAALFETLHNSMSINLCFTVTVNNHNYA.....
NPY2R_chicken  FVGFVTVVDFEFTVVEVKRHHYLAALFETLHNSMSINLCFTVTVNNHNYA.....
NPY2R_rat       FVGFVTVVDFEFTVVEVKRHHYLAALFETLHNSMSINLCFTVTVNNHNYA.....
HGRBPMY14      LKTLHNVSLILAIISAYETVETVIVVREKRTFCGQVWVDDQVLYSSVETVIFGCI
human_gpcr_dJ60N4_3
gpcr73_mouse   LKTLHNVSLILAIISAYETVETVIVVREKRTFCGQVWVDDQVLYSSVETVIFGCI
NPY2R_chicken  LKTLHNVSLILAIISAYETVETVIVVREKRTFCGQVWVDDQVLYSSVETVIFGCI
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Figure 3

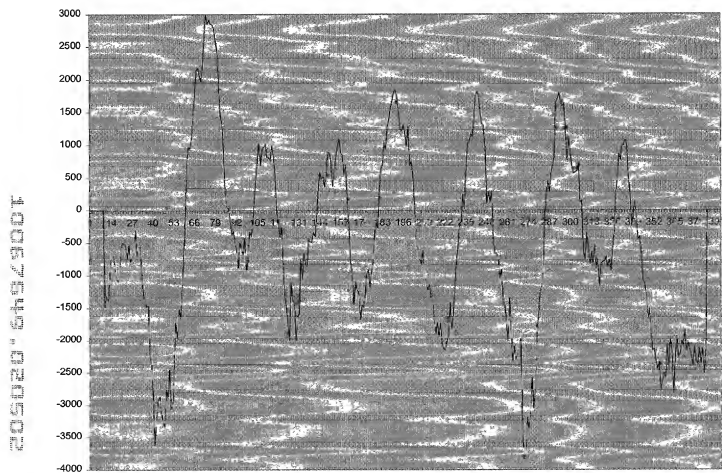
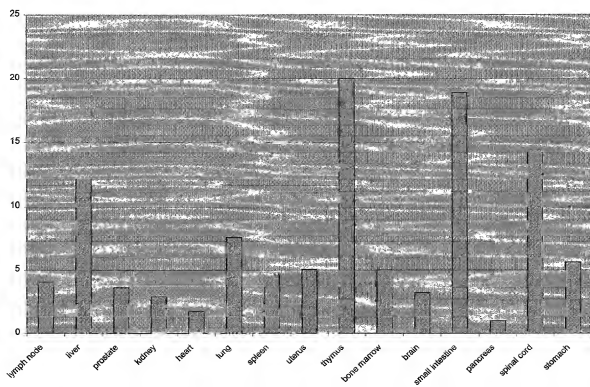


Figure 4



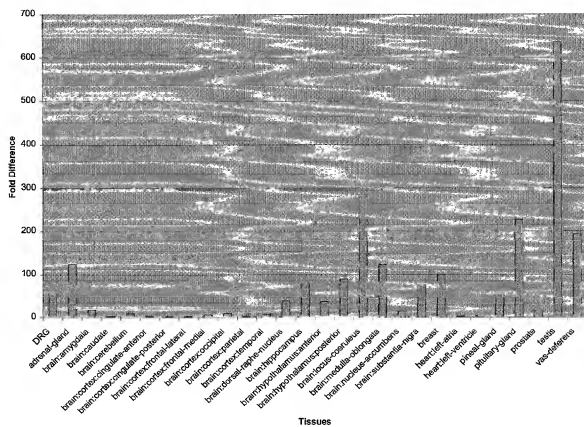
202509.6492901

Figure 5.

<u>Protein</u>	<u>Genbank ID</u>	<u>Identities</u>	<u>Similarities</u>
human dj680N4.3 G-protein coupled receptor	gi 7688218	90%	93%
mouse G-protein coupled receptor GPR73 protein	gi 7248884	84%	88%
chicken neuropeptide Y receptor Y2 protein	gi 11545537	27%	39%
rat neuropeptide Y/peptide YY- Y2 receptor protein	gi 10281748	29%	41%

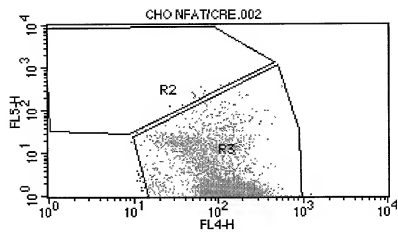
10067649-020502

Figure 6



10067549.020502

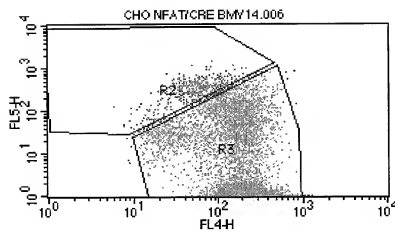
Figure 7



205520.64929001

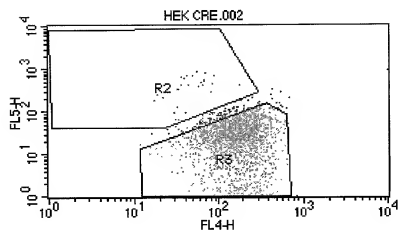
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Figure 8



2005020.67929007

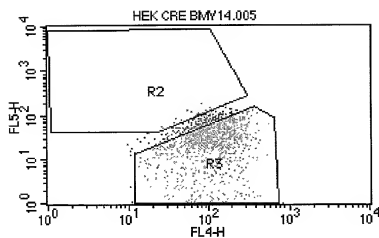
Figure 9



209020-649/9007

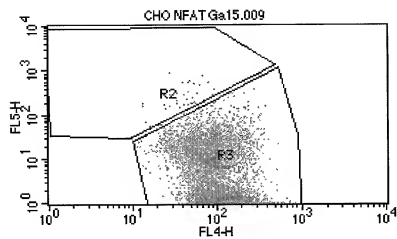
10067649-020502

Figure 10



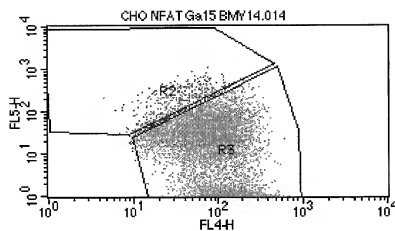
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Figure 11



205020-61929001

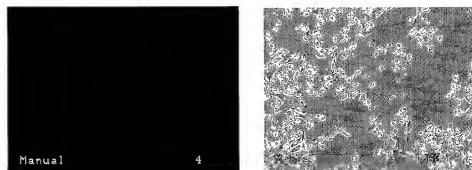
Figure 12



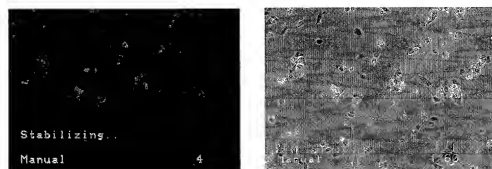
205020* 6492900T

Figure 13

Cho NFAT Ga15 Control (Fluorescent vs. Bright Field)



Cho NFAT Ga15 BMY14 (Fluorescent vs. Bright Field)



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Figure 14

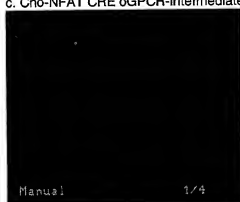
a. Cho-NFAT CRE



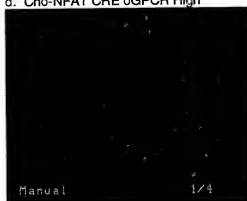
b. Cho-NFAT CRE + F/T/P



c. Cho-NFAT CRE oGPCR-Intermediate



d. Cho-NFAT CRE oGPCR High



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Figure 15

VDTF F EDIPWGFVLF	(SEQ ID NO:87)
LFV DKWDL S NFWGGG	(SEQ ID NO:88)
LFLE AWDL S DTPHLY	(SEQ ID NO:89)
VWGNSLI VGRW DVVG	(SEQ ID NO:90)
IGGV GDGLYVVS WDL	(SEQ ID NO:91)

1.0087649.020502